G2P workshop dictionary for PCC - December 2005, Updated June 2006.

Term	Definition
Activation tag lines	Plants that have been *transformed* with a foreign gene promoter. If this promoter integrates into the plant's native DNA such that it resides near a gene contained in the DNA, then transcription of that native gene will be activated. Consequently, the plant is expressing a gene that may not normally be expressed at these levels or under these conditions. In this way, one can determine the effect of expression of this gene on the plant, and begin to understand the function of the gene.
ACE	This refers to the 'Allowable Cut Effect' in forestry when additional harvesting is permitted in mature stands based on the expectation of additional growth in younger stands (eg: when tree improved stock has been planted).
Adaptation	Genetic changes, in response to natural selection, by which populations adjust to their environment.
Adapted material	Material resulting from natural evolution, or breeding and testing, that is capable of adequate growth and reproduction in a given habitat and that will not have adverse impacts on the health, functioning and productivity of the ecosystem.
Additive genetic effects	The effects of alleles at two different loci are additive when their combined effect is equal to the sum of their individual effects. Additive effects are most easily understood in the context of continuous (quantitative) traits. Consider a disease in which two loci, locus 1 with alleles A and a, and locus 1 with alleles B and b, contribute to the phenotype. If each allele represented by a capital letter contributes a score of 2 to the phenotype, and each allele represented by a small letter contributes a score of 3 to the phenotype, then if the alleles at loci 1 and 2 are additive, the resultant pheno-types for the possible genotypes are as follows: AABB - 8; AABb - 9; Aabb - 11; AaBB - 10; AaBb - 10; Aabb - 11; aaBB -10; aaBb - 9; aabb - 12.
Afforestation	The establishment of a tree *crop* on an area from which the crop has always been absent, or absent for a very long time.
AFLP	Amplified fragment length polymorphism. This is a laboratory technique used to generate *molecular markers* for discriminating across genotypes. Essentially, the *DNA* isolated from a plant is digested into smaller fragments using *restriction enzymes*; this digested DNA is then amplified by *PCR* using specially-designed *primers,* and the results visualized on a gel.
Allele	One of two or more alternate forms of the gene, differing in DNA sequence and affecting the functioning of a single gene product (RNA and/or protein). All alleles of a series occupy the same site or locus on a pair of homologous chromosomes.
Amplified family	An aggregate of multiple vegetative propagules from each of several to many members of a half- or full-sib family.
Annotation	A commentary, description, definition or index associated with a given gene or protein sequence that provides information pertaining to the sequence, structure, and function of the gene and/or protein coded for by the gene. Such information may be derived by computer-based studies of the sequence or experimental-based studies of the gene or protein.
Antisense	A piece of nucleic acid, typically created in the lab, which has a sequence exactly opposite to an mRNA molecule made by the body. mRNA molecules made by the body serve as templates for the synthesis of protein (see transcription). Since the "antisense" mRNA molecule binds tightly to its mirror image, it can prevent a particular protein from being made.
Arabidopsis	*Arabidopsis thaliana*; Shepard's purse. A plant species that is used in laboratory research in a manner analogous to the use of lab rats in medical sciences. This plant species exhibits many traits that make it easy to work with under laboratory conditions, and as such, many genetic and genomic resources have been created for Arabidopsis.
Bacterial artificial chromosome (BAC)	A vector used to clone DNA fragments (100- to 300-kb insert size; average, 150 kb) in Escherichia coli cells.
Backcross	A cross between a plant that is heterozygous for alleles obtained from two parental strains and a second from one of those parental strains. Also used to describe the breeding protocol of an outcross followed by a backcross.
Base pair	Two nitrogenous bases (adenine and thymine or guanine and cytosine) held together by weak bonds. Two strands of DNA are held together in the shape of a double helix by the bonds between base pairs.
Base population	The population of trees from which individuals are chosen to establish the breeding population and/or production population. Generally refers to a wild population.
Biodiversity	The variety and variability among living organisms and ecosystems of which they are part. It has three components – ecosystem diversity, species diversity and genetic diversity.

Bioinformatics	The collection, organization and analysis of large amounts of biological data, using networks of computers and databases. Historically, bioinformatics concerned itself with the analysis of the sequences of genes and their products (proteins), but the field has since expanded to the management, processing, analysis and visualization of large quantities of data from genomics, proteomics, drug screening and medicinal chemistry. Bioinformatics also includes the integration and “mining” (detailed searching) of the ever-expanding databases of information from these disciplines. An enterprise wide bioinformatics solution includes an internal database system, feeds and links to external (public, collaborative) databases, a middle tier of software that defines the biological objects of interest to the researcher, an algorithm tier where the analysis and mining tools reside, and a user tier where the user can access, integrate, manipulate and visualize the data in a variety of ways.
Breeding	The science and art of changing the genetic constitution of a population of plants and animals.
Breeding population	A set of trees within which crosses are made to generate material for the next cycle of selection. Breeding populations are generally large, as compared to the production population.
Breeding value (BV)	The genetic value of an individual for a given trait, based on the mean performance of its offspring or other relatives. BV may be expressed in terms of measurement units such as m or cm; it is more commonly expressed in relative terms, as a percent deviation from the population mean.
Cavitation	The formation of air bubbles in the water column of tracheary elements of the xylem, which develop from dissolved air in the water column. Air bubbles that form break the continuity of the water column, which disrupts water movement to the tissues served by those conducting elements.
cDNA	DNA molecule synthesized in the laboratory using RNA as a template. This is accomplished using a viral enzyme called reverse transcriptase
cDNA Library	A collection of DNA sequences that code for genes. The sequences are generated in the laboratory from mRNA sequences.
Centromere	The central structure of a *chromosome.*
Chloroplast chromosome	Circular DNA found in the photosynthesizing organelle (chloroplast) of plants instead of the cell nucleus where most genetic material is located.
Chromosome	A microscopic, generally threadlike or rodlike body consisting of linear segments of deoxyribonucleic acid (DNA) carrying the genes and forming the primary constituent of the cell nucleus.
Climax forest	The final stage in a forest succession sequence where the species composition remains relatively unchanged as long as climate and physical geography remain the same.
Clinal or Clinal Variation	A continuous character gradient, usually assumed to be genetically controlled, with geography and environment. Adjacent populations merge into one another with regard to character expression with no sharp breaks.
Clonal test	A genetic test designed to evaluate a set of clones.
Clonal propagation	The wide-scale reproduction of selected clones, while maintaining their individual identity.
Clone	An individual or group of individuals reproduced asexually from a single organism and therefore genetically identical to the parent/progenitor.
Cloning	In biotechnology, obtaining a group of genetically identical cells from a single cell; making identical copies of a gene.
Cloning vector	DNA molecule originating from a virus, a plasmid, or the cell of a higher organism into which another DNA fragment of appropriate size can be integrated without loss of the vector's capacity for self-replication; vectors introduce foreign DNA into host cells, where the DNA can be reproduced in large quantities. Examples are plasmids, cosmids, and yeast artificial chromosomes; vectors are often recombinant molecules containing DNA sequences from several sources.
Coding content	A term that is generally used to refer to the portion of a DNA or RNA sequence that provides the sequence information used to synthesize a protein. Coding content can refer to the regions of a single gene that provide the template that ultimately is reflected in the sequence of the protein product of the gene. Coding content can also refer to the regions across a chromosome or within an entire genome that define protein sequences. In the narrow sense of the term, the coding content of the genome is only the portions of genes that ultimately are reflected in the mRNA serving as a template for protein synthesis. In the broad sense of the term, the coding content of the genome can be used to refer to all the genes within a genome.
Codon	A set of three nucleotide bases in a DNA or RNA sequence, which together code for a unique amino acid. For example, the set AUG (adenine, uracil, guanine) codes for the amino acid methionine.
Contig	Group of cloned (copied) pieces of DNA representing overlapping regions of a particular chromosome.

Diploid	A full set of genetic material consisting of paired chromosomes, one from each parental set. Most animal cells except the gametes have a diploid set of chromosomes. Some plant species may have multiple sets of chromosomes, a situation known as polyploidy.
Dioecious	Refers to a species in which male and female "flowers" generally occur on different plants; thus each plant is usually either male or female, but not both; e.g. aspen *(Populus tremuloides)* .
Domain	This refers to different regions within the province of Quebec.
Dominant allele	An allele that is almost always expressed, even if only one copy is present.
Down regulation	A decrease in the rate or manner in which a gene is expressed. This decrease in *transcription* often leads to a decrease in the amount of protein synthesized. Compare with upregulation.
Ecosystem	A complex interacting system that includes all plants, animals, and their environment within a particular area.
Endangered	"A wildlife species that is facing imminent extirpation or extinction" (from the Species at Risk Act).
Epistasis	One gene interferes with or prevents the expression of another gene located at a different locus.
Expressed sequence tag (EST)	A short strand of DNA (approximately 200 base pairs long) which is part of a cDNA. Because an EST is usually unique to a particular cDNA, and because cDNAs correspond to a particular gene in the genome, ESTs can be used to help identify unknown genes and to map their position in the genome.
Ex situ	A method of conservation in which components of biodiversity are conserved outside of the site, away from the natural habitat.
Exon	The portion(s) of a gene that contain sequence that is reflected in the mature messenger RNA used as the template for protein synthesis. Within a gene, exons can be interrupted by introns (see definition for intron). In other words, exons are the coding portions of genes.
Exotic	An introduced species, hybrid or population not native to an area.
Facile transformation	The ability to perform genetic transformation easily and quickly.
Filial Generation (F1, F2)	Each generation of offspring in a breeding program, designated F1, F2, etc.
Fitness	The relative ability of organisms of a particular genotype to survive and produce offspring, or the contribution of one of a pair of alleles to the general vigour of an organism.
Functional Genomics	The use of genetic technology to determine the function of newly discovered genes by determining their role in one or more model organisms. Functional genomics uses as its starting point the isolated gene whose function is to be determined, and then selects a model organism in which a homolog of that gene exists. This model organism can be as simple as a yeast cell or as complex as a nematode worm, fruitfly, plant or even a mouse. The gene is selectively inactivated or "knocked out" using a variety of genetic techniques, and the effect of its selective deletion on that organism is determined. By knocking out a gene in this way, its contribution to the function of the organism (and, by implication, its function in man), can be determined. Functional genomics has proven particularly useful as a means of validating or testing novel therapeutic targets. In another approach, a whole set of genes may be systematically inactivated and the effect of this on a particular cellular function examined. Here, a new gene and its function are identified simultaneously.
Forest 2020	A short term program funded by the Federal Government to promote the planting of hybrid poplars across Canada. See Government of Canada web site for more details. Program ended Spring 2006.
Gene	The fundamental physical and functional unit of heredity, responsible for specific traits such as eye color. A gene is an ordered sequence of nucleotides located in a particular position on a particular chromosome that encodes a specific functional product (i.e., a protein or RNA molecule). A gene is written in a code of four letters: A, C, T and G, representing four chemicals, and depending on the gene, these letters are repeated a certain number of times. The smallest human gene contains 252 repetitions of these letters, while the longest one repeat them more than a million times. There are approximately 30,000 genes in the human genome.
Gene chip	Development of cDNA microarrays from a large number of genes. Used to monitor and measure changes in gene expression for each gene represented on the chip.
Gene flow	The movement of genes (*i.e.* alleles) within a population or between interbreeding populations as a result of outcrossing and natural selection or seed migration.
Gene expression	The process by which a gene's coded information is converted into the structures present and operating in the cell. Expressed genes include those that are transcribed into mRNA and then translated into protein and those that are transcribed into RNA but not translated into protein (e.g., transfer and ribosomal RNAs).
Gene family	Genes within an organism that are similar in sequence, and likely have arisen from the same ancestral gene. Genes classified together in the same family can code for proteins that often have similar functions.

Gene library	A collection of cloned DNA fragments which, taken together, represent the entire genome of a specific organism. Such libraries or "gene banks" are assembled so as to allow the isolation and study of individual genes. Gene libraries are produced by first breaking up or "fractionating" an entire genome. This fractionation can be accomplished either by physical methods or by use of restriction enzymes. The genome fragments are then cloned (multiplied in number) and stored for later use.
Gene pool	The totality of genes and their alleles within an interbreeding population.
Genecology	The study of the genetics of the populations of plants in relation to the ecological niches they occupy or it is the study of adaptive properties of the populations in relation to their environments.
Genetic diversity	In a group such as a population or species, the possession of a variety of genetic traits that frequently result in differing expressions in different individuals. The variation of genes within a species; it is the material upon which the agents of evolution act. Loss of variation may prevent adaptive change in populations of a species and reduce their ecological fitness.
Genetic gain	The average heritable change attributable to selection in a given trait, from one generation to the next.
Genetic load	The accumulation of genetic mutations over-time. This occurs in particularly long-lived species such as conifers and clonal aspen.
Genetic map	A map of the genes along the chromosomes of an organism based on surrogates that identify genes - traditionally phenotypes (e.g. the round or wrinkled seeds of Mendel) but more commonly now molecular markers such as SSRs or SNPs. Genetic maps are constructed in pedigrees using the laws of inheritance (see *Genetics*)
Genetic polymorphism	A difference in DNA sequence among individuals, groups, or populations (e.g. a genetic polymorphism might give rise to blue eyes versus brown eyes, or straight hair versus curly hair). Genetic polymorphisms may be the result of chance processes, or may have been induced by external agents (such as viruses or radiation). If a difference in DNA sequence among individuals has been shown to be associated with disease, it will usually be called a genetic mutation. Changes in DNA sequence which have been confirmed to be caused by external agents are also generally called "mutations" rather than "polymorphisms."
Genetic sequence	The succession of nucleotides that make up a strand of DNA. The four nucleotides that make up DNA are adenine (A), guanine (G), cytosine (C) and thymine (T). The particular succession of these nucleotides in a particular DNA strand give the DNA its uniqueness.
Genetic variation	Differences displayed by individuals within a species which may be favoured or eliminated by natural or artificial selection. In sexual reproduction, reshuffling of genes through recombination in each generation ensures the maintenance of variation. The ultimate source of variation is mutation which produces fresh genetic material.
Genetic worth	For a seed or vegetative lot, the predicted difference in value of a given trait (e.g. height or volume) from the value of that trait in wild stand material.
Genetics	The study of heritability of traits (characteristics) and the mechanisms that control the expression of genes that are responsible for the traits.
Genetically modified organism (GMO)	An organism that, through human intervention in a laboratory, has had its genome, or genetic code, deliberately altered through the insertion of a specific identified sequence of genetic coding material (generally DNA) that has been either manufactured or physically excised from the genome of another organism. Genetic modification may be used to alter any of a wide range of traits, including insect and disease resistance, herbicide tolerance, tissue composition and growth rate.
Genome	A genome is all the DNA in an organism, including its genes. Genes carry information for making all the proteins required by all organisms. These proteins determine, among other things, how the organism looks, how well its body metabolizes food or fights infection, and sometimes even how it behaves. DNA is made up of four similar chemicals (called bases and abbreviated A, T, C, and G) that are repeated millions or billions of times throughout a genome. The human genome, for example, has 3 billion pairs of bases. The particular order of As, Ts, Cs, and Gs is extremely important. The order underlies all of life's diversity, even dictating whether an organism is human or another species such as yeast, rice, or fruit fly, all of which have their own genomes and are themselves the focus of genome projects.
Genomics	The study of large numbers of genes, or in some cases all genes in an organism. Genomics includes the cataloguing of large numbers genes by DNA sequencing, studying the expression of large numbers of genes simultaneously, and studying variation in large numbers of genes. Compare with molecular biology, where one or a few genes are studied at one time.
Genotype	The genetic identity or constitution of an individual. Physical material, in the form of plant tissue, provides the medium for storage and transmission of a genotype.
Germplasm assembly	Archiving living plant materials at a single location. The materials usually represent at least partially the genetic diveristy of the plant or group of plants.
Habitat	The natural environment in which an organism or population lives. Habitat may refer to all of the organisms and their physical environment in a particular place.

Haploid	A single set of chromosomes (half the full set of genetic material) present in the egg and sperm cells of animals and in the egg and pollen cells of plants.
Haplotype	In diploid organisms (most plants and animals), each chromosome has two homologous copies (2N). The sequences of the copies are distinct, unless the organism has been extensively inbred. Haplotype (from haploid, or the 1N state) refers to the DNA sequence of one of the two homologous chromosomes.
Heterosis	The gain in fitness or speed of growth often observed in the progeny of crosses between genetically distinct individuals (or in some cases species, as in hybrid poplars).
Heterozygosity	The presence of different alleles at one or more loci on homologous chromosomes.
Heritability	The degree to which a trait is controlled in advanced generations in a genetic cross by inheritance of specific alleles of genes (as opposed to, for example, environmental influences)
Homologue	A character (e.g. gene) that is related to another character through evolution from a common ancestor
Homology	A term that describes the relationship between two characters (e.g. genes), where the two characters have arisen (i.e. diverged) from a common ancestor.
Homozygote	An organism that has two identical alleles of a gene.
Hybrid	The progeny of genetically different parents. Often display *heterosis* .
Hybrid orchard	An orchard including non-hybrid parents that is managed to produce hybrid seed. This term does not apply to orchards that include naturally occurring hybrid parents (e.g. Sw x Se).
Hybridization	The processes of cross-mating individuals or populations that are genetically different.
In silico	Computational analysis of data sets to make predictions about gene structure, relationships or function.
In situ	A method of gene conservation where genetic resources are conserved on site within the natural habitat.
Inactivation	Loss of the ability of gene to function (i.e. produce an active protein), often based on insertion of a piece of foreign DNA that disrupts the gene.
Indels	A type of genetic mutation in which there is an insertion of one or more nucleotides or a deletion of one or more nucleotides within a DNA sequence. A DNA sequence with an insertion is therefore longer than a sequence that does not, and a DNA sequence that has a deletion is therefore shorter than a sequence that does not. Molecular markers can be designed to detect indels, and thus indels are valuable features in genetic analysis.
Introgression or Introgressive hybridization	The incorporation of genes of one species into the gene pool of another. If the ranges of the two species overlap and fertile hybrids are produced, they tend to backcross with the more abundant species. This process results in a population of individuals most of who resemble the more abundant parents but who possess also some characters of the other parental species.
Intron	Introns are the non-coding portions of a gene that are interspersed within exons (see definition of exon). Both introns and exons are initially transcribed as a single RNA molecule, i.e. introns appear in the RNA strand that is synthesized from the DNA template; however, introns are subsequently clipped (spliced) out of the RNA prior to the RNA being used as a template for protein synthesis.
Line	Plants regenerated from an independent *transformation* event. Because DNA that is introduced into the plant by transformation may 1. not integrate into the genome (and thus be lost), 2. insert into an infinite number of points in the genome (which may lead to different effects) or 3. lead to the insertion of multiple copies of the DNA in the genome, plants from each transformation event must be considered independently. Each of these independent events is considered a line.
Linkage group	A genetically inferred chromosome, consisting of mapped genes or molecular markers that are inherited as a unit. Used synonymously with chromosome, except that the physical chromosome associated with the linkage group is difficult or impossible to visualize by microscopy (as for most poplar chromosomes).
Linkage map	A map of the relative positions of genetic loci on a chromosome, determined on the basis of how often the loci are inherited together.
Locus	The position on a chromosome of a gene or other chromosome marker; also, the DNA at that position. The use of locus is sometimes restricted to mean expressed DNA regions.
LVL	This refers to Laminated Veneer Lumber.
Mapping population	A group of conspecific organisms sharing a common gene pool used in the construction of a genetic map.
Markers	Differences in DNA, RNA, or protein sequence that can be used to distinguish between two or more genetically distinct individuals.

Mass spectrometry	An instrument used to identify chemicals in their pure state or in a complex mixture by their mass and charge. In proteomics MS is used to accurately measure the mass of protein fragments (peptides), thus allowing them to be accurately assigned to a protein predicted from the genome.
Messenger RNA (mRNA)	The DNA of a gene is transcribed (see transcription) into mRNA molecules, which then serve as a template for the synthesis of proteins.
Metabolite	organic (carbon, hydrogen, oxygen-containing) compounds synthesized by an organism, that are used to carry out many diverse functions in a cell. There are many classes of metabolites, including amino acids, hormones, carbohydrates, terpenoids, alkaloids, cell wall compounds, and lipids.
metabolomic	The study of many metabolites simultaneously.
Microarray	Miniature spots of molecules on a glass slide that may be reacted with a solution of other molecules to simultaneously study the state of thousands of arrayed molecules at once. MIcroarrays may be DNA fragments, antibodies, or proteins, but most commonly consist of DNA fragments representing all or a large fraction of the genome of an organism (e.g. 15,000 elements representing 15,000 poplar genes). DNA microarrays are used to measure the expression of thousands of genes at once.
Microsatellite (SSR)	A common DNA polymorphism consisting of differing numbers of short repeated nucleotides. For example, one allele may have the microsatellite, or SSR (simple sequence repeat) "CCC", while another may be "CC". Such DNA poly morphisms can be easily tested using molecular methods.
Mill creep	The ongoing increase in fibre requirement needs for a facility that are a consequence of capital and engineering improvements over time. These increases in fibre requirements are often related to capital improvements that may address product quality, process reliability, or environmental concerns, yet are justified
Model system	A organism that has biological and practical advantages allowing fundamental biological processes to be easily studied. Because of the genetic relatedness of organisms and conservation of basic processes between organisms, information from "models" can often be applied to organisms less easy to study.
Molecular marker	A difference in DNA sequence between two alleles (alternative forms of a gene or DNA sequence) that can be easily identified using molecular biology techniques. See *microsatellite, SNP.*
Monoecious	Refers to a species in which male and female “flower” parts generally occur on the same plant, either within a single “flower” or separately; thus each plant is usually both male and female; e.g. white spruce *(Picea glauca)* .
Motif	A conserved amino acid sequence that identifies a region of a protein conserved in large numbers of other proteins. Usually has biological significance, e.g. region of a protein involved in DNA binding, enzyme function, or interaction with other proteins.
Mutation	The process by which a gene undergoes a structural change; a modified gene resulting from mutation.
Natural range	Range of natural distribution of a taxon, excluding any portion that is the result of introduction to a region.
Natural selection	The process by which the genetic makeup of a population changes under natural conditions, without human interference, on the basis of its ability to become better adapted, survive or reproduce in a particular set of environmental conditions.
Negative betas	performance. The term negative betas is often used to describe stocks or portfolios that move in the opposite direction of the market. This type of stock or investment can be useful to diversify or construct portfolios that reduce risk.
Nucleotide	The "building block" of nucleic acids, such as the DNA molecule. A nucleotide consists of one of four bases - adenine, guanine, cytosine, or thymine - attached to a phosphate-sugar group. In DNA the sugar group is deoxyribose, while in RNA (a DNA-related molecule which helps to translate genetic information into proteins),
NUE Nutrient use efficiency	A relative measure of plant productivity as a function of nutrient consumption. In general, only one nutrient at a time is considered, and the concept is most often applied to nitrogen. NUE can be expressed in many different ways; the most general of these is the amount of dry matter produced per unit of nutrient applied.
Orthologue	Genes of same function found in two different organisms.
Over expression	Over production of a gene product (protein) brought about by genetic manipulation to deregulate activity of the gene (for example by fusing the gene to a very strong *promoter,* and reintroducing into the organism).
Pedigree	A record of parentage, sometimes also including data on the performance of parents and other relatives.

PFRA	Prairie Farm Rehabilitation Administration, located in Indian Saskatchewan is part of Agriculture and Agri-Food Canada – PFRA Agroforestry Division.
Phenology	The study of timing of periodic phenomena such as flowering, growth initiation, growth cessation, etc. especially as related to seasonal changes in temperature, photoperiod, etc.
Phenotype	The sum total of the environmental and genetic (hereditary) influences on a tree; the visible characteristics of a plant.
Phylogenetics	The relationships of organisms to each other based on DNA and/or gene sequences.
Physical map	As opposed to a *genetic map* , provides sequence of clones of DNA (physical DNA) along linkage groups or chromosomes. The poplar genome sequence integrates the genetic map with the physical map with the DNA sequence contained within the physical DNA clones.
Pipeline	The workflow between tasks within a large project, that collectively permit development of an application or knowledge that could not have been produced by any of the individual tasks.
Plant community	A group of ecologically related populations of various species that occur in a particular geographic area at a particular time.
Plants with Novel Traits	A plant variety/genotype possessing characteristics that demonstrate neither familiarity nor substantial equivalence to those present in a distinct, stable population of a cultivated species of seed in Canada and that have been intentionally selected, created or introduced into a population of that species through a specific genetic change. In this definition, familiarity means, the knowledge of the characteristics of a plant species and experience with the use of that plant species in Canada and substantial equivalence means, the equivalence of a novel trait within a particular plant species, in terms of its specific use and safety to the environment and human health, to those in that same species, that are in use and generally considered as safe in Canada, based on valid scientific rationale.
Plasmid DNA	Circular DNA molecule from bacteria that is separate and distinct from the circular chromosome. Foreign genes can be inserted into plasmids in the laboratory, and used to *transform* bacteria so that the bacteria now contains the foreign gene. This allows for mass production of the genes, and facilitates working with them.
Plieotropy	Multiple phenotypes or traits caused by mutation or variation in a single gene
Polymerase Chain Reaction	(PCR) A laboratory technique for multiplication of a quantity of a specific DNA sequence via an enzymatic reaction in vitro, rather than multiplication of a biological organism possessing the DNA sequence. The reaction relies on use of a DNA template of the sequence of interest, and primers (short DNA sequences) that match either end of the DNA template. The enzyme used in PCR can use these primers as the starting point to synthesize a DNA strand that is the exact copy of the template. With every cycle of amplification, there is a new copy of DNA made for each template present in the solution, i.e. the amount of DNA doubles with every cycle. Thus, there is exponential production of DNA with multiple cycles.
Polymorphism	Difference in DNA sequence among individuals that may underlie differences in health. Genetic variations occurring in more than 1% of a population would be considered useful polymorphisms for genetic linkage analysis.
Population	A group of individuals of the same species that occupy a particular geographic area or region. In general, individuals within a population interbreed and exchange genes with each other.
Probe	Single-stranded DNA or RNA molecules of specific base sequence, labelled either radioactively or immunologically, that are used to detect the complementary base sequence by hybridization.
Promoter	The DNA regulatory elements that control gene activity (expression), usually located upstream of the protein coding part of a gene.
Propagule	A live entity capable of producing a new mature individual (*e.g.* , a cutting, graft, tissue culture explant).
Proteome	Proteins expressed by a cell or organ at a particular time and under specific conditions.

Proteomics	The study of the full set of proteins encoded by a genome.
Provenance	The original geographic source of seed or other propagules. Also, the test population resulting from seed collected from a particular location.
Quantitative trait	A phenotype that can vary in a quantitative manner when measured among different individuals. The variation in expression can be due to combinations of genetic and environmental factors, as well as chance. Quantitative traits are often controlled by the cumulative action of alleles at multiple loci.
QTL Quantitative trait loci	Regions on a linkage group or chromosome that contain one or more genes that control quantitative traits, that is traits that that are measured by quantity (amount of growth, degree of drought tolerance, timing of fall senescence, etc).
Ramet	An individual that has been vegetatively reproduced from the original plant, or *ortet* , and is thus genetically identical to it.
Ramet, grafted	A ramet created by grafting a twig or bud from the original plant onto a physically distinct rootstock. The portion of the grafted ramet above the graft union is genetically identical to the original plant (See also “Ramet, rooted.”)
Ramet, rooted	A ramet created by rooting a twig or cutting from the original plant. The whole ramet is genetically identical to the original plant (See also, “Ramet, grafted.”)
Reads	Short (~200-800 base pairs) stretches of DNA sequence data generated from the ends of longer fragments by a DNA sequencing machine.
Reclamation	A planned series of activities designed to recreate the biophysical capacity of an ecosystem.
Recessive allele	An allele which will only result in a specific phenotype when its counterpart allele is also recessive, or when no counterpart allele exists.
Reforestation	The reestablishment of trees on denuded forest land by natural or artificial means such as planting and seeding.
Regulatory gene	A gene which controls the protein-synthesizing activity of other genes.
Regulatory region	Similar to a *promoter,* a region of DNA associated with a gene that controls the activity (expression) of the gene.
Restriction enzyme	A protein that recognizes specific, short nucleotide sequences and cuts DNA at those sites. Bacteria contain over 400 such enzymes that recognize and cut more than 100 different DNA sequences.B40
Restriction fragment length polymorphism	Variation between individuals in DNA fragment sizes cut by specific restriction enzymes; polymorphic sequences that result in RFLPs are used as markers on both physical maps and genetic linkage maps. RFLPs usually are caused by mutation at a cutting site.
Rolling front orchard	A *seed orchard* in which individual trees or groups of trees of known breeding value are replaced on a more or less continuous basis as new material of higher breeding value becomes available.
Rootling	A plant derived from a section of root, typically found with aspen production. A root mass is cut into small pieces, each piece is planted in soil and a shoot suckers from a bud on the root section.
Scaffold	An assembled set of shorter genomic DNA sequences that overlap with each other and are presumed to represent a discrete region of the genome. Ultimately, all sequence scaffolds should coalesce into a subset equivalent to the number of chromosomes.
Section (land)	A parcel of land that is 1 mile by 1 mile, equalling 640 acres or 256 hectares.
Seed orchard	A stand of trees, usually several hundred to several thousand in number, established and managed primarily for early and abundant production of seed for deployment. Trees in the orchard are derived and propagated from selected parent trees by grafting or by seed.
Segregation	The property of genes on a given chromosome (and the traits they specify) to move together, or segregate together, in progeny of a genetic cross.
Serial propagation	The propagation of multiple clonal copies of a plant through repeated cycles of collection of vegetative units (e.g. scions or cuttings), creation of new plants from these units, and vegetative growth of the derived plants, without returning to the original plant. Also known as “bulking up” or multiplication.
Shotgun sequencing	Sequencing method that involves randomly sequenced cloned pieces of the genome, with no foreknowledge of where the piece originally came from. This can be contrasted with "directed" strategies, in which pieces of DNA from known chromosomal locations are sequenced. Because there are advantages to both strategies, researchers use both random (or shotgun) and directed strategies in combination to sequence genomes.
Signal transduction	A relay of biochemical events that is triggered in a cell upon perception of an environmental or internal cue, resulting in changes to gene expression and/or the activities of proteins within the cell.
Single nucleotide polymorphism	DNA sequence variations (polymorphisms) that occur when a single nucleotide (A, T, C, or G) in the genome sequence is different in one *allele* or *haplotype* of the two homologous chromosomes.

Splicing	The removal of introns from the sequence of mRNA. When an mRNA molecule is synthesized from a DNA template, introns are transcribed (see transcription) along with exons. In the splicing process, this material is cut out and the exons are joined together to form a continuous coding sequence.
Steckling	A plant (tree) derived from rooting a sucker generated from a section of root, typically found with aspen production. However, any rooted cutting could be refered to as a steckling (eg: yellow cedar, hybrid poplar).
Stoolbed	An aggregation of closely spaced stumps, or stools, managed for the production of one-year-old vegetative sprouts (whips). Harvested whips are used for operational planting stock and can be pre-rooted prior to deployment.
Sunscald	A condition that arises when sunlight heats the stem of dormant trees during the winter, either directly or via reflection off of the snow (albedo effect). The heating of the stem induces cellular activity within the cambial meristem; cold evening temperatures will generally kill these activated cells, resulting in damage to the cambium and bark.
Sylleptic branching	This occurs when lateral buds grow out during the same season in which they are formed without an intervening rest or winter dormancy period. Sylleptic branching may significantly enhance the number of branches, leaf area and total growth of a tree particularly when it is young. Very little is known about the physiology of sylleptic branching although in stoolbeds, fertilizer appears to have an effect on the amount of sylleptic branching in some clones.
Taxa (singular "taxon")	The general term for taxonomic groups of whatever rank.
Telomere	The ends of chromosomes.
TFL Tree Farm Licence	Tree Farm Licence is an operational area designed for forestry use and held by an industrial stakeholder. Land designated under the Forest Act that is managed for sustainable timber harvest, as determined by an allowable annual cut. TFLs typically combine public (provincial Crown) land with private land and timber licences. A TFL has a term of 25 years. (Adapted from MoF, Glossary of Forestry Terms. http://www.for.gov.bc.ca/hfd/library/documents/glossary/) Source: http://www.for.gov.bc.ca/hfp/sof/pdf/glossary.pdf
Threatened	“A wildlife species that is likely to become an endangered species if nothing is done to reverse the factors leading to its extirpation or extinction” (from the Species at Risk Act).
Tiling path	The overlapping arrangement of DNA clones in a *physical map* along a linkage group.
Tilling	A new method for detecting single nucleotide polymorphisms (SNPs) within a gene.
Translation	The process during which the information in mRNA molecules is used to construct proteins.
Transcript	The messenger RNA produced as a copy of a gene.
Transcription	The synthesis of an RNA copy from a sequence of DNA (a gene); the first step in gene expression.
Transcription factor	A protein with the function of regulating the expression (transcription of DNA into RNA) of other genes in the genome. Usually binds to DNA in the *promoter* or r*egulatory region*, and may affect traits by affecting activity of multiple other genes.
Transcriptome (see proteome)	The complete set of transcribed genes in a genome at a given time during development or after environmental stimulation.
Transposable element	A class of DNA sequences that can move from one chromosomal site to another.
Transformation	Introduction of foreign DNA into a plant, so that the plant now can manufacture the product that is encoded by the DNA.
Tree Improvement	The tree selection, evaluation and breeding for more desirable characteristics, such as faster growth, drought, disease or insect resistance.
Unigene set	A collection of gene sequences in which each sequence is distinct from all others in the collection.
Up regulation	An increase in the rate or manner in which a gene is expressed. This decrease in *transcription* often leads to an increase in the amount of protein synthesized. Compare with downregulation.
Veneer ribbon	A veneer ribbon is the results of the log peeling process for the production of engineered wood products, e.g. plywood. The ribbon is a continous (ideally), uniform thickness sheet of wood that is removed from the log by a blade, and then clipped to size before layup.
WUE Water use efficiency	A relative measure of plant productivity as a function of water consumption. WUE can be expressed as the amount of dry matter produced per volume of water lost via transpiration. WUE can also be expressed at the level of the leaf as the ratio of the rate of photosynthesis to the rate of water transpiration.
Wild	Genetic materials of native species originating from natural regeneration.
Wild population	A population within its natural range in which the individuals are the result of natural reproduction.

Wild-type	Trees that have not been genetically modified.
Xylem	The tissue making up wood in the tree. In the case of poplar, xylem consists mainly of vessel members (which join end-to-end to create the water-conducting elements), fibres, and ray cells.

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